wherein a group comprises sequencing reads from one of the uniquely labeled double-stranded target nucleic acid molecules; and

(e) comparing the first-strand sequencing reads with the second-strand sequencing reads in each group, and generating an error-corrected sequence for a plurality of the double-stranded target nucleic acid molecules by distinguishing erroneous nucleotides in one strand that lack a matched base change in the complementary strand.

40. The method of claim **39**, wherein the double-stranded cyphers comprise random identifier sequences.

41. The method of claim **39**, wherein the double-stranded cyphers comprise identifier sequences that are not completely random.

42. The method of claim **39**, wherein a target tag sequence comprises nucleotides at an end of a target nucleic acid molecule.

43. The method of claim **42**, wherein the end of the target nucleic acid molecule is a sheared end.

44. The method of claim **39**, wherein the random or partially-random identifier sequence is double-stranded.

45. The method of claim **39**, wherein the identifier sequence is at an end of the double-stranded cypher.

46. The method of claim **39**, wherein the target tag sequence is 5 nucleotides to 20 nucleotides in length.

47. The method of claim **39**, wherein each of the cyphers are unique.

48. The method of claim **39**, wherein the erroneous nucleotides comprise a polymerase error that arose during amplification or sequencing.

49. The method of claim **39**, wherein the plurality of target nucleic acid molecules comprise a mutation present at a frequency of 2.1×10^{-6} or lower.

50. The method of claim **39**, further comprising detecting a cancer biomarker in one of the error-corrected sequences, wherein the cancer biomarker comprises a nucleotide mutation.

51. The method of claim **39**, further comprising using the error-corrected sequences to assess cancer response to therapy.

52. The method of claim **39**, wherein the sample is derived from a human subject having cancer, and wherein the method further comprises detecting in one of the error-corrected sequences a mutation that confers to the cancer resistance to cancer therapy.

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